Amendments to the claims:

1. – 62. (Cancelled)

63. (Currently Amended) An intracellular recognition molecule R, comprising a proteinaceous recognition domain, conformationally constrained by covalent bonding to a platform, said recognition molecule R specifically interacting, within a cell, with a site on a predetermined intracellular target molecule T, the interaction with T occurring with an affinity corresponding to a K_d value ~~of less than or equal to 5×10^{-9} M~~ comprised between 1×10^{-9} M and 1×10^{-14} M, wherein said intracellular recognition molecule R is a peptide aptamer, wherein said platform is thioredoxin (TRX) or a TRX-like protein, and wherein the proteinaceous recognition domain consists of a peptide having a length of five to sixty amino acids.

64. (Previously Presented) The intracellular recognition molecule R according to claim 63 wherein the recognition domain consists of a peptide having a length of ten to forty amino acids.

65. (Previously Presented) The intracellular recognition molecule R according to claim 64 wherein the peptide recognition domain comprises a random peptide.

66. (Cancelled)

67. (Previously Presented) The intracellular recognition molecule R according to claim 64, wherein the platform is heterologous with respect to the recognition domain.

68. – 69. (Cancelled)

70. (Previously Presented) The intracellular recognition molecule according to claim 63, wherein the intracellular target molecule T with which R specifically interacts is chosen from a cyclin-dependent kinase and a pro-apoptotic protein.

71. (Previously Presented) The intracellular recognition molecule according to claim 70 wherein the intracellular target molecule T is Cdk2.

72. (Previously Presented) The intracellular recognition molecule according to claim 71 wherein the peptide recognition domain comprises a mutant of the amino acid sequence QVWSLWALGWRWLRRYGWNM (SEQ ID NO:1), said mutant having from one to three amino acid changes with respect to said sequence.

73. (Previously Presented) The intracellular recognition molecule according to claim 72 wherein the peptide recognition domain comprises the amino acid sequence QVWSSWALGWRWLRRYGWGM (SEQ ID NO:2).

74. (Previously Presented) The intracellular recognition molecule according to claim 70 wherein the intracellular target molecule T is Bax.

75. (Previously Presented) The intracellular recognition molecule according to claim 74 wherein the peptide recognition domain comprises a mutant of the amino acid sequence PRGAPMWMRWVCQMLETMFL(SEQ ID NO:3), said mutant having from one to three amino acid changes with respect to said sequence.

76. (Previously Presented) The intracellular recognition molecule according to claim 75 wherein the peptide recognition domain comprises the amino acid sequence PRGAPMWLRCVCQMLETKFL(SEQ ID NO:4).

77. (Previously Presented) An oligomeric intracellular recognition molecule, comprising from two to four intracellular recognition molecules R, each being an

intracellular recognition molecule according to claim 63, said recognition molecules being covalently linked to each other, either directly or via a linker.

78. (Previously Presented) The oligomeric intracellular recognition molecule according to claim 77 comprising two intracellular recognition molecules R.

79. – 83. (Cancelled)

84. (Previously Presented) The intracellular recognition molecule R according to claim 63 wherein the recognition domain consists of 20 amino acids.

85. (Previously Presented) An intracellular recognition molecule R, comprising a proteinaceous recognition domain, conformationally constrained by covalent bonding to a platform, said recognition molecule R specifically interacting, within a cell, with a site on a predetermined intracellular target molecule T, the interaction with T occurring with an affinity corresponding to a K_d comprised between 5×10^{-9} M and 1×10^{-14} M, wherein said intracellular recognition molecule R is a peptide aptamer, wherein said platform is thioredoxin (TRX), a human thioredoxin, or a glutaredoxin and wherein the proteinaceous recognition domain consists of a peptide having a length of five to sixty amino acids.

86. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the intracellular target molecule T with which R specifically interacts is chosen from a cyclin-dependent kinase and a pro-apoptotic protein.

87. (Previously Presented) The intracellular recognition molecule according to claim 86, wherein the intracellular target molecule T is Cdk2.

88. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the peptide recognition domain comprises a mutant of the amino acid sequence QVWSLWALGWRWLRRYGWNM (SEQ ID NO:1), said mutant having from one to three amino acid changes with respect to said sequence.

89. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the peptide recognition domain comprises the amino acid sequence QVWSSWALGWRWLRRYGWGM (SEQ ID NO:2).

90. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the intracellular target molecule T is Bax.

91. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the peptide recognition domain comprises a mutant of the amino acid sequence PRGAPMWMRWVCQMLETMFL(SEQ ID NO:3), said mutant having from one to three amino acid changes with respect to said sequence.

92. (Previously Presented) The intracellular recognition molecule according to claim 85, wherein the peptide recognition domain comprises the amino acid sequence PRGAPMWLRCVCQMLETKFL(SEQ ID NO:4).